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☐ 1: [P54725](#). UV excision repai...[gi:1709983]

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LOCUS            P54725                            363 aa                    linear    PRI 15-SEP-2003  
 DEFINITION    UV excision repair protein RAD23 homolog A (HHR23A).  
 ACCESSION    P54725  
 VERSION      P54725    GI:1709983  
 DBSOURCE     swissprot: locus R23A\_HUMAN, accession P54725;  
               class: standard.  
               created: Oct 1, 1996.  
               sequence updated: Oct 1, 1996.  
               annotation updated: Sep 15, 2003.  
               xrefs: gi: [498145](#), gi: [498146](#), gi: [1905905](#), gi: [1905912](#), gi:  
               [23664449](#), gi: [23664450](#), gi: [33878469](#), gi: [15559329](#), gi: [1082759](#),  
               pdb accession 1DV0, pdb accession 1F4I, pdb accession 1IFY  
               xrefs (non-sequence databases): GenewHGNC:9812, MIM [600061](#),  
               GOGO:0003697, GOGO:0006289, InterProIPR004806, InterProIPR006636,  
               InterProIPR000449, InterProIPR000626, PfamPF00627, PfamPF00240,  
               SMARTSM00727, SMARTSM00165, SMARTSM00213, TIGRFAMsTIGR00601,  
               PROSITEPS50030, PROSITEPS50053  
 KEYWORDS     DNA damage; DNA repair; Nuclear protein; 3D-structure; Repeat;  
               Polymorphism.  
 SOURCE       Homo sapiens (human)  
       ORGANISM   [Homo sapiens](#)  
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE    1    (residues 1 to 363)  
       AUTHORS    Masutani,C., Sugasawa,K., Yanagisawa,J., Sonoyama,T., Ui,M.,  
                   Enomoto,T., Takio,K., Tanaka,K., van der Spek,P.J., Bootsma,D.,  
                   Hoeijmakers,J.H.J. and Hanaoka,F.  
       TITLE       Purification and cloning of a nucleotide excision repair complex  
                   involving the xeroderma pigmentosum group C protein and a human  
                   homologue of yeast RAD23  
       JOURNAL     EMBO J. 13 (8), 1831-1843 (1994)  
       MEDLINE     [94222030](#)  
       PUBMED      [8168482](#)  
       REMARK      SEQUENCE FROM N.A.  
 REFERENCE    2    (residues 1 to 363)  
       AUTHORS    Lamerdin,J.E., McCready,P.M., Stilwagen,S., Ramirez,M. and  
                   Carrano,A.  
       TITLE       Direct Submission  
       JOURNAL     Submitted (~MAR-1997)  
       REMARK      SEQUENCE FROM N.A.  
 REFERENCE    3    (residues 1 to 363)  
       AUTHORS    Rieder,M.J., Livingston,R.J., Daniels,M.R., Montoya,M.A.,  
                   Chung,M.-W., Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L.,  
                   Robertson,P.D., Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and  
                   Nickerson,D.A.  
       TITLE       Direct Submission  
       JOURNAL     Submitted (~OCT-2002)

REMARK SEQUENCE FROM N.A., AND VARIANTS ALA-131 AND MET-200.  
REFERENCE 4 (residues 1 to 363)  
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,  
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,  
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,  
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,  
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,  
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,  
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,  
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,  
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,  
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,  
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,  
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,  
Butterfield,Y.S.N., Krzywinski,M.I., Skalska,U., Smailus,D.E.,  
Schnerch,A., Schein,J.E., Jones,S.J.M. and Marra,M.A.  
TITLE Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
MEDLINE [22388257](#)  
PUBMED [12477932](#)  
REMARK SEQUENCE FROM N.A.  
TISSUE=Pancreas  
REFERENCE 5 (residues 1 to 363)  
AUTHORS Dieckmann,T., Withers-Ward,E.S., Jarosinski,M.A., Liu,C.F.,  
Chen,I.S. and Feigon,J.  
TITLE Structure of a human DNA repair protein UBA domain that interacts  
with HIV-1 Vpr  
JOURNAL Nat. Struct. Biol. 5 (12), 1042-1047 (1998)  
MEDLINE [99061330](#)  
PUBMED [9846873](#)  
REMARK STRUCTURE BY NMR OF 319-363.  
REFERENCE 6 (residues 1 to 363)  
AUTHORS Withers-Ward,E.S., Mueller,T.D., Chen,I.S. and Feigon,J.  
TITLE Biochemical and structural analysis of the interaction between the  
UBA(2) domain of the DNA repair protein HHR23A and HIV-1 Vpr  
JOURNAL Biochemistry 39 (46), 14103-14112 (2000)  
MEDLINE [20541363](#)  
PUBMED [11087358](#)  
REMARK STRUCTURE BY NMR OF 319-363.  
COMMENT -----  
This SWISS-PROT entry is copyright. It is produced through a  
collaboration between the Swiss Institute of Bioinformatics and  
the EMBL outstation - the European Bioinformatics Institute.  
The original entry is available from <http://www.expasy.ch/sprot>  
and <http://www.ebi.ac.uk/sprot>  
-----  
[FUNCTION] Involved in postreplication repair of UV-damaged DNA.  
Postreplication repair functions in gap-filling of a daughter  
strand on replication of damaged DNA (Potential).  
[SUBUNIT] Interacts with MJD.  
[SUBCELLULAR LOCATION] Nuclear (Probable).  
[DOMAIN] The ubiquitin-like domain mediates interaction with MJD.  
[SIMILARITY] Contains 1 ubiquitin-like domain.  
[SIMILARITY] Contains 2 UBA domains.  
FEATURES Location/Qualifiers

source 1..363  
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gene 1..363  
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/product="UV excision repair protein RAD23 homolog A"  
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/note="T -> A. /FTid=VAR\_016251."  
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/note="UBA 1."  
Region 200  
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/note="T -> M. /FTid=VAR\_016252."  
Region 318..358  
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/region\_name="Domain"  
/note="UBA 2."  
Region 321..324  
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Region 325..331  
/gene="RAD23A"  
/region\_name="Hydrogen bonded turn"  
Region 334..341  
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Region 342..345  
/gene="RAD23A"  
/region\_name="Hydrogen bonded turn"  
Region 348..354  
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/region\_name="Helical region"  
Region 355..356  
/gene="RAD23A"  
/region\_name="Hydrogen bonded turn"

## ORIGIN

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241 fqnmrqviqq npallpallq qlgqenpql qqisrhqeqf iqmlneppge ladisdvege
301 vgaigeeapq mnyiqvtpqe keaierlkal gfpeslviqa yfaceknenl aanflsqnf
361 dde
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